Nucleotide   "Exhibit C"

Alphabet of Life

Display Settings: GenBank

Porcine G protein gene, exon 1

GenBank: M57287.1

FASTA   Graphics

Features Sequence

```
LOCUS       PIGI2AA                 983 bp    DNA     linear   MAM 27-APR-1993
DEFINITION  Porcine G protein gene, exon 1.
ACCESSION   M57287                  ◄——
VERSION     M57287.1  GI:164496
KEYWORDS    G protein.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 983)
  AUTHORS   Holtzman,E.J., Soper,B.W., Stow,J.L., Ausiello,D.A. and Ercolani,L.
  TITLE     Regulation of the G-protein alpha i-2 subunit gene in LLC-PK1 renal
            cells and isolation of porcine genomic clones encoding the gene
            promoter
  JOURNAL   J. Biol. Chem. 266 (3), 1763-1771 (1991)   ◄——
   PUBMED   1899094
FEATURES             Location/Qualifiers
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                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
     CDS             646..712
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                     /product="G protein"
                     /protein_id="AAA31052.1"
                     /db_xref="GI:164496"
                     /translation="MIDKNLREDGEKAAREVKLLLL"
     intron          713..>983
ORIGIN
        1 atcccaaaac aagtttattg ggttcattaa ctttaacaaa tgacgaagac acgcctcctc
       61 tactcatctc gctcgactct cagaagcttg gagggctggt tcctgcttgg cccgcgaggt
      121 gcaccggatc ctcatcctcg ggctacgaga tccgcccgcc cccgccgtcg ggcagcggag
      181 ctccaggcgc tccgcaccca atcggagccc ggccccgcct gcgatcaaag cttctgtgct
      241 aggctctacc cctacagcta tcccttggcg tggctccgcc ttcacgcccgc accgagtttg
      301 ggctgcgcct aacttctccc tcgagccaat cactgacccc gggtctcctg tggcccgcc
      361 tccgggcccg ccccggccca gtcctcggcc agactagctc gggcccacc cccggccgc
      421 cctgccgtcg gtgcgcggcg gcctggaagg caccgcctgc agacgctcgg aactgcggac
      481 ccgagagcta cccgtagagg gccggcggcg gcgggagccg agtgggtcgg gcggggccga
      541 gccgggccgg ggccgtgtgg tggccgggca gcggccggcg ggcggacggg ccgggatgggc
      601 tgcaccgtga gcgctgagga caaggcggcg gccgagcgct ccaaaatgat cgacaagaac
      661 ctgcgggaag acggcgagaa ggcggcgcgg gaggtgaagt tgctgctctt gggtgaggcc
      721 gcgtcctgcg ctgggacccc tgattcccta cccaaattcc ctactttgac ctgcggacta
      781 gtgtttcgaa ctcccacact cggcctggac ttaacccgt agacccgcct ggcaaggaca
      841 tacaaataaa taatggatca aaactcaggg ttggcctaga cctctcagat ccagagccca
      901 gactctagat cagactcaac tcatcccaaa ccccgggccc ccaaacccag acactggtgc
      961 ctcaacatcc gctgcccaga att
//
```

BLAST

Basic Local Alignment Search Tool

- •

Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

dbj|DD249890| (3871 letters)

Results for: [*dbj|DD249890.1 Gm1 promoter and use thereof.(3871bp) ▼]

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
> gi|99025749|dbj|DD249890.1|　　←—
> gi|99025749|dbj|DD249890.1|
Description
> Gm1 promoter and use thereof.
Molecule type
> dna
Query Length
> 3871

Subject ID
> gi|164496|gb|M57287.1|PIGI2AA　　←—
Description
> Porcine G protein gene, exon 1
Molecule type
> nucleic acid
Subject Length
> 983
Program
> BLASTN 2.2.24+ Citation

Reference
Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

⇒ • No significant similarity found. For reasons why,click here

Other reports: Search Summary [Taxonomy reports]

Search Parameters

Search parameter name Search parameter value

| Program | blastn |

Word size	28
Expect value	10
Hitlist size	100
Match/Mismatch scores	1,-2
Gapcosts	0,0
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Karlin-Altschul statistics

Params Ungapped Gapped

Lambda	1.33271	1.28
K	0.620991	0.46
H	1.12409	0.85

Results Statistics

Results Statistics parameter name Results Statistics parameter value

Effective search space	3737433

Graphic Summary

Distribution of Blast Hits on the Query Sequence

[?] _____

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

10/593,216	Gm1 promoter and use thereof	09-17- 2010::10:01:28

Supplemental Content - Search Results

This page gives you information about the number of versions associated with the application you requested. Use this page to obtain specific version information

Version Number	Item Id	Item Size
1	09323b6780c8016e	42.752
1	09323b6780c8016f	42.752
1	② 09323b6780c80170	42.752
1	09323b6780c80171	42.752
1	① 09323b6780c80172	42.752
1	09323b6780c80173	42.752
1	09323b6780c80174	42.752
1	09323b6780c80175	42.752
1	09323b6780c80176	42.752
1	09323b6780c80177	42.752
1	09323b6780c80178	42.752
1	09323b6780c80179	42.752

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